

Figure 1A: Nucleotide and amino acid sequences (SEQ ID Nos: 1 and 2) of the ATP/ADP translocase from *Chlamydia pneumoniae*

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gaaataaaaa actatcagaa tagaaaataa aagtatttca gagggtaa atg aca      56
                                     Met Thr
                                     1

aaa acc gaa gaa aaa cct ttt gga aaa ttg cgc tct ttc ttg tgg ccg    104
Lys Thr Glu Glu Lys Pro Phe Gly Lys Leu Arg Ser Phe Leu Trp Pro
      5                      10                      15

ata cat act cac gag cta aag aaa gtt ctg cca atg ttc cta atg ttc    152
Ile His Thr His Glu Leu Lys Lys Val Leu Pro Met Phe Leu Met Phe
      20                      25                      30

ttc tgt att aca ttt aac tat acg gtg tta cgc gat aca aaa gac act    200
Phe Cys Ile Thr Phe Asn Tyr Thr Val Leu Arg Asp Thr Lys Asp Thr
      35                      40                      45                      50

ctt att gtg gga gct cct ggt tct ggt gca gag gca ata cct ttc atc    248
Leu Ile Val Gly Ala Pro Gly Ser Gly Ala Glu Ala Ile Pro Phe Ile
                      55                      60                      65

aag ttt tgg ctt gtt gtc ccc tgt gct att atc ttt atg ctt att tat    296
Lys Phe Trp Leu Val Val Pro Cys Ala Ile Ile Phe Met Leu Ile Tyr
                      70                      75                      80

gca aag cta agt aat att tta agt aag cag gcc tta ttt tat gca gtg    344
Ala Lys Leu Ser Asn Ile Leu Ser Lys Gln Ala Leu Phe Tyr Ala Val
      85                      90                      95

gga acg ccc ttt tta att ttc ttt gcc ctg ttc ccg act gta att tat    392
Gly Thr Pro Phe Leu Ile Phe Phe Ala Leu Phe Pro Thr Val Ile Tyr
      100                      105                      110

ccg cta cgc gat gtt tta cat cct aca gaa ttt gct gac cgt tta cag    440
Pro Leu Arg Asp Val Leu His Pro Thr Glu Phe Ala Asp Arg Leu Gln
      115                      120                      125                      130

gcc atc cta cct cca gga ttg cta gga ctg gtt gcc atc tta aga aac    488
Ala Ile Leu Pro Pro Gly Leu Leu Gly Leu Val Ala Ile Leu Arg Asn
                      135                      140                      145

tgg aca ttt gct gca ttt tat gta ctt gct gaa cta tgg gga agc gtc    536
Trp Thr Phe Ala Ala Phe Tyr Val Leu Ala Glu Leu Trp Gly Ser Val
                      150                      155                      160

atg cta tct cta atg ttc tgg gga ttt gct aat gaa att aca aaa atc    584
Met Leu Ser Leu Met Phe Trp Gly Phe Ala Asn Glu Ile Thr Lys Ile
                      165                      170                      175

cac gaa gca aag cgt ttc tac gct ctt ttc ggt atc gga gct aat att    632
His Glu Ala Lys Arg Phe Tyr Ala Leu Phe Gly Ile Gly Ala Asn Ile
      180                      185                      190
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## ANNOTATED SHEET SHOWING CHANGES

Title: CHLAMYDIA ANTIGENS AND  
CORRESPONDING DNA FRAGMENTS AND  
USES THEREOF

Inventor(s): Andrew D. MURDIN et al.

Appl. No.: 09/869,433

Figure 1B (Continued Continuation of Figure 1)

ctt	tta	cta	gct	tct	ggg	cgt	gca	att	gtt	tgg	gct	tca	aag	ttg	aga	680
Ser	Leu	Leu	Ala	Ser	Gly	Arg	Ala	Ile	Val	Trp	Ala	Ser	Lys	Leu	Arg	
195					200					205					210	
gct	tcc	gtt	tct	gaa	ggg	gta	gat	cct	tgg	gga	att	tct	tta	cgt	ctt	728
Ala	Ser	Val	Ser	Glu	Gly	Val	Asp	Pro	Trp	Gly	Ile	Ser	Leu	Arg	Leu	
				215					220					225		
ttg	atg	gct	atg	act	att	gta	tct	gga	ctt	gtt	ctt	atg	gcc	agt	tac	776
Leu	Met	Ala	Met	Thr	Ile	Val	Ser	Gly	Leu	Val	Leu	Met	Ala	Ser	Tyr	
				230				235					240			
tgg	tgg	atc	aat	aag	aac	gta	ttg	acc	gat	cct	cgc	ttc	tat	aat	cca	824
Trp	Trp	Ile	Asn	Lys	Asn	Val	Leu	Thr	Asp	Pro	Arg	Phe	Tyr	Asn	Pro	
		245					250					255				
gaa	gaa	atg	caa	aag	ggg	aaa	aaa	ggg	gct	aaa	cct	aaa	atg	aat	atg	872
Glu	Glu	Met	Gln	Lys	Gly	Lys	Lys	Gly	Ala	Lys	Pro	Lys	Met	Asn	Met	
		260				265					270					
aaa	gat	agc	ttc	ctc	tat	ctt	gat	aga	tct	cct	tat	att	ctt	tta	tta	920
Lys	Asp	Ser	Phe	Leu	Tyr	Leu	Asp	Arg	Ser	Pro	Tyr	Ile	Leu	Leu	Leu	
					280					285					290	
act	ctc	ttg	gtt	att	gcc	tat	ggg	att	tgc	att	aac	tta	atc	gaa	gtg	968
Thr	Leu	Leu	Val	Ile	Ala	Tyr	Gly	Ile	Cys	Ile	Asn	Leu	Ile	Glu	Val	
				295					300					305		
act	tgg	aaa	agt	cag	ctg	aaa	ctg	caa	tat	cct	aat	atg	aat	gac	tat	1016
Thr	Trp	Lys	Ser	Gln	Leu	Lys	Leu	Gln	Tyr	Pro	Asn	Met	Asn	Asp	Tyr	
			310					315					320			
agt	gag	ttc	atg	ggg	aac	ttc	tcc	ttc	tgg	act	ggc	gta	gta	tcc	gta	1064
Ser	Glu	Phe	Met	Gly	Asn	Phe	Ser	Phe	Trp	Thr	Gly	Val	Val	Ser	Val	
		325					330					335				
ctt	atc	atg	cta	ttt	gtt	ggg	ggg	aac	gtc	att	cgt	aaa	ttt	gga	tgg	1112
Leu	Ile	Met	Leu	Phe	Val	Gly	Gly	Asn	Val	Ile	Arg	Lys	Phe	Gly	Trp	
		340				345					350					
tta	act	gga	gcc	cta	gtc	act	cct	gtc	atg	gtt	ctc	cta	aca	ggg	atc	1160
Leu	Thr	Gly	Ala	Leu	Val	Thr	Pro	Val	Met	Val	Leu	Leu	Thr	Gly	Ile	
		355				360				365					370	
gtt	ttc	ttc	gct	ctt	gtt	atc	ttt	aga	aac	caa	gct	tct	ggg	ctg	gtc	1208
Val	Phe	Phe	Ala	Leu	Val	Ile	Phe	Arg	Asn	Gln	Ala	Ser	Gly	Leu	Val	
				375					380					385		
gct	atg	ttc	ggg	aca	act	cct	ctc	atg	cta	gct	gtg	gtt	gtc	gga	gct	1256
Ala	Met	Phe	Gly	Thr	Thr	Pro	Leu	Met	Leu	Ala	Val	Val	Val	Gly	Ala	
			390					395					400			
ata	cag	aat	att	ctt	tcg	aaa	tcc	aca	aaa	tac	gct	ctc	ttt	gac	tca	1304
Ile	Gln	Asn	Ile	Leu	Ser	Lys	Ser	Thr	Lys	Tyr	Ala	Leu	Phe	Asp	Ser	
		405					410						415			

Figure 1C (~~Continued~~ Continuation of Figure 1)

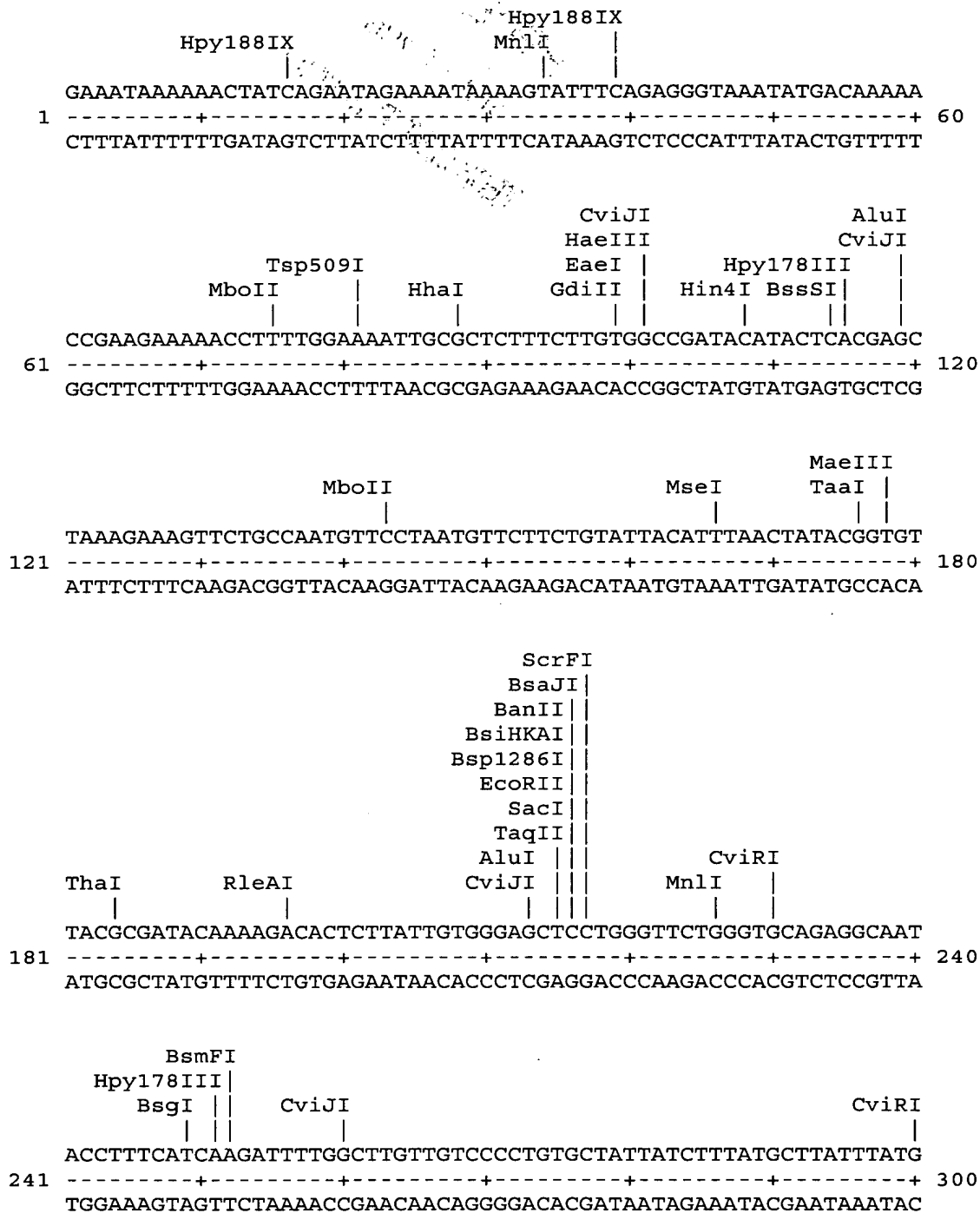
act aaa gaa atg gcc tat atc cct ctt gac caa gag caa aaa gtc aaa	1352
Thr Lys Glu Met Ala Tyr Ile Pro Leu Asp Gln Glu Gln Lys Val Lys	
420 425 430	
ggt aag gct gct att gat gta gtt gcc gcc cgc ttc gga aaa tca gga	1400
Gly Lys Ala Ala Ile Asp Val Val Ala Ala Arg Phe Gly Lys Ser Gly	
435 440 445 450	
gga gct tta atc caa caa ggt ttg ctc gtt atc tgt gga agt att gga	1448
Gly Ala Leu Ile Gln Gln Gly Leu Leu Val Ile Cys Gly Ser Ile Gly	
455 460 465	
gct atg acc cct tat ctt gca gtg att ctt ctt ttc atc att gct att	1496
Ala Met Thr Pro Tyr Leu Ala Val Ile Leu Leu Phe Ile Ile Ala Ile	
470 475 480	
tgg ttg gtt tct gca act aag tta aac aaa cta ttc tta gcg cag tct	1544
Trp Leu Val Ser Ala Thr Lys Leu Asn Lys Leu Phe Leu Ala Gln Ser	
485 490 495	
gct ctt aaa gaa caa gaa gtg gct caa gaa gat tca gct cct gct tct	1592
Ala Leu Lys Glu Gln Glu Val Ala Gln Glu Asp Ser Ala Pro Ala Ser	
500 505 510	
tca tagagttgct tctcttactc ttgttgatcc ctacctgctt tt	1637
Ser	
515	



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Figure 2A: Restriction enzyme analysis of the *C. pneumoniae* ATP/ADP translocase gene.

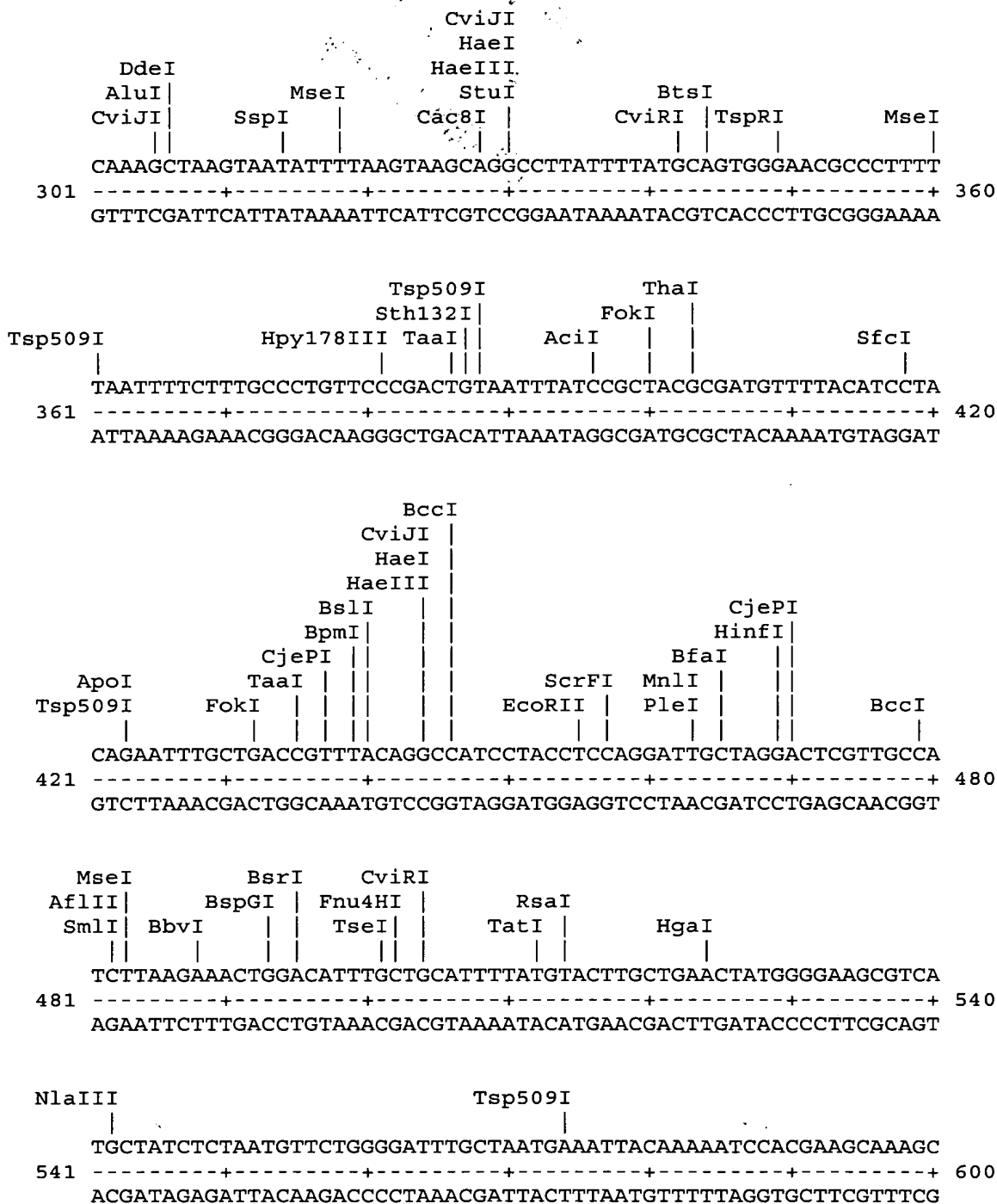




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Figure 2B (Continued Continuation of Figure 2)

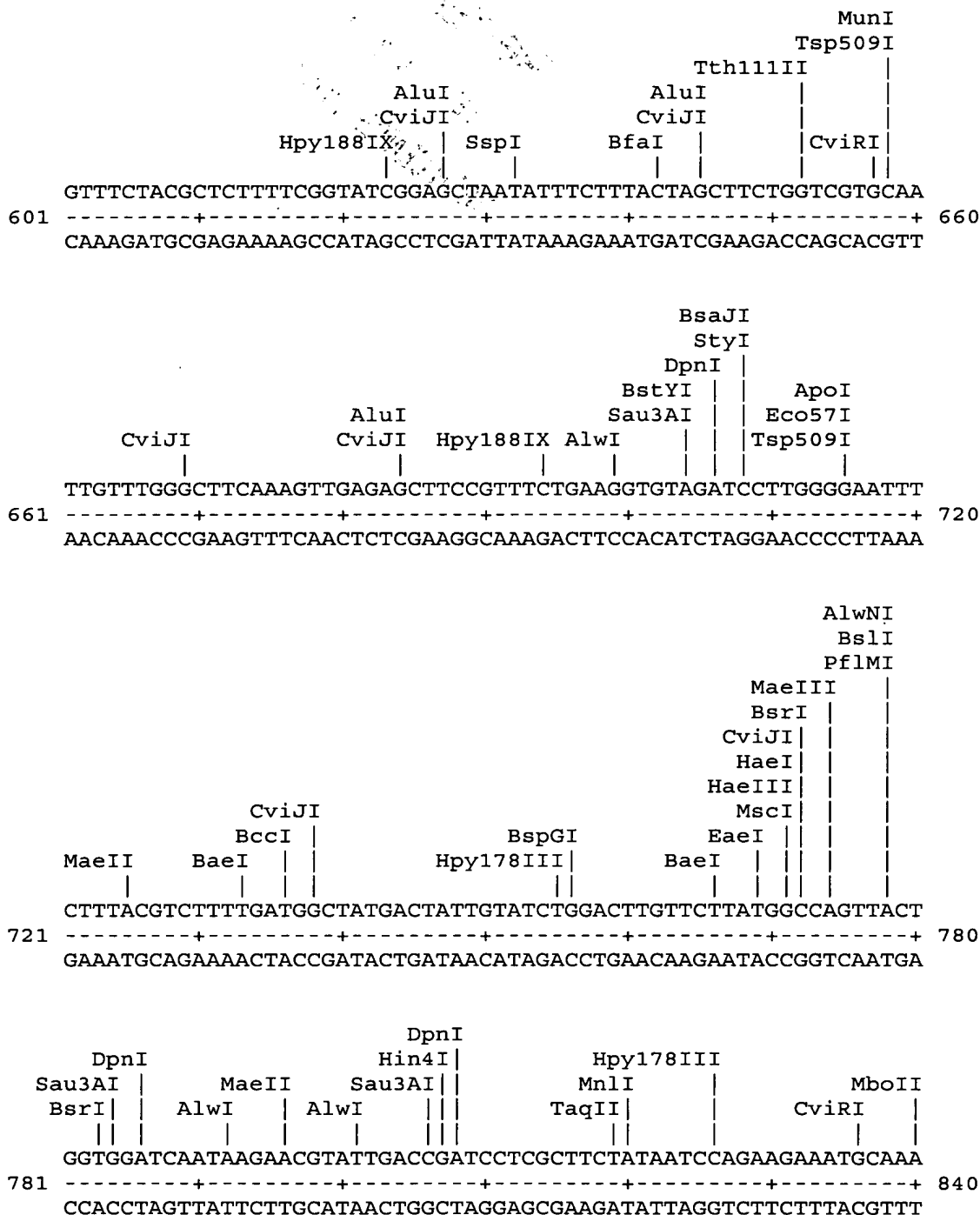




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Figure 2C (Continued Continuation of Figure 2)

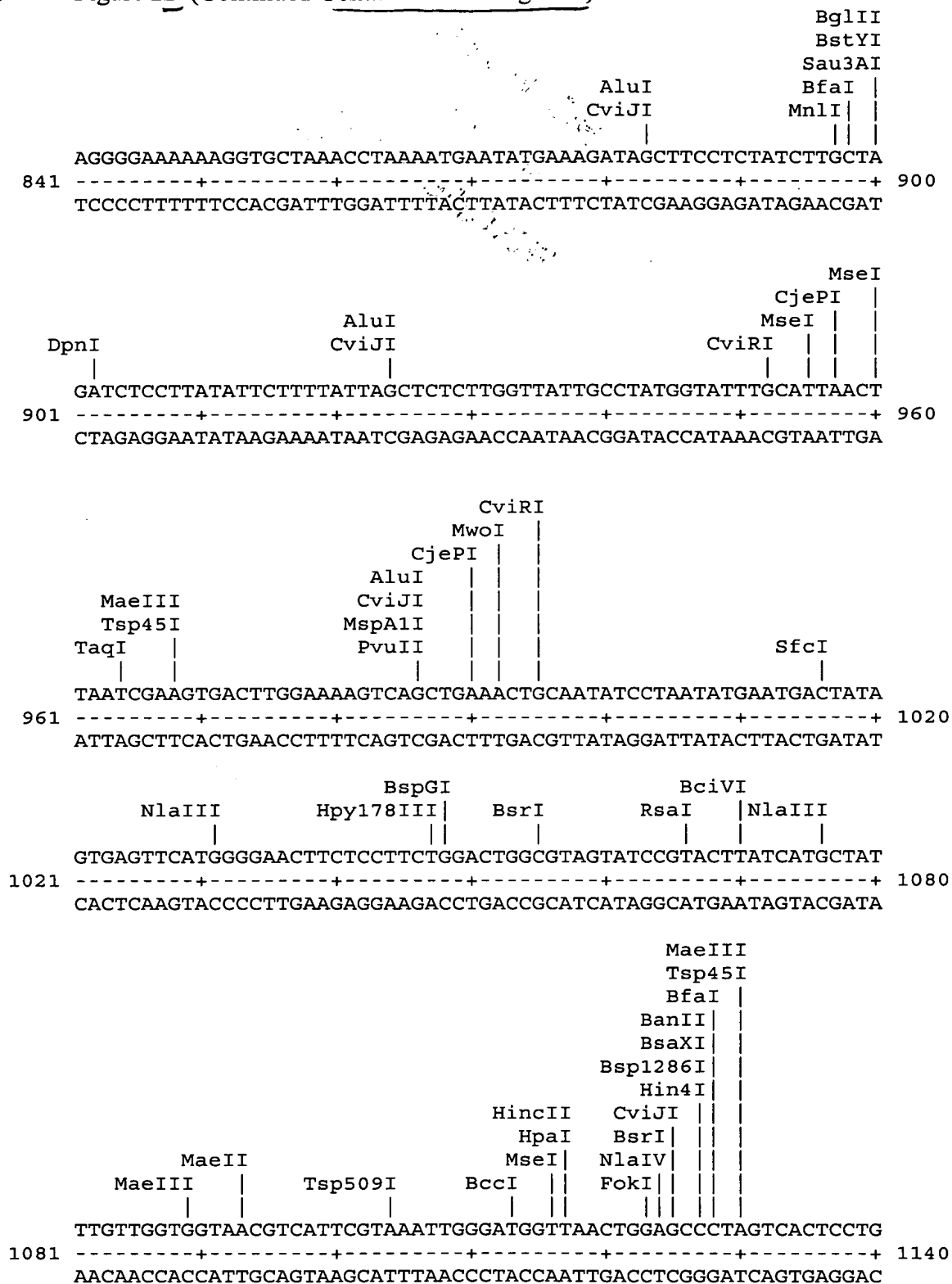




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Figure 2D (Continued Continuation of Figure 2)





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Figure 2E (Continued Continuation of Figure 2)

